

SEQUENCE LISTING

<110> Bachmann, Martin  
Vogt, Lorenz

<120> Immune Modulatory Compounds and Methods

<130> 1700.0390002

<150> 60/408,233

<151> 2002-09-06

<150> 60/449,583

<151> 2003-02-26

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<170> PatentIn version 3.2

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Tyr Pro Ile Leu Ala Leu Val Gly Glu Glu Val Glu Phe Pro Cys His	
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Ala Gln Asp Leu Phe Ser Leu Glu Thr Ser Val Val Val Arg Ala Gly	
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Pro Glu Tyr Pro Ile Leu Ala Leu Val Gly Glu Glu Val Glu Phe Pro 45 50 55  
tgc cac cta tgg cca cag ctg gat gcc cag caa atg gag atc cgc tgg 243  
Cys His Leu Trp Pro Gln Leu Asp Ala Gln Gln Met Glu Ile Arg Trp 60 65 70  
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Phe Arg Ser Gln Thr Phe Asn Val Val His Leu Tyr Gln Glu Gln Gln 75 80 85 90  
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Ile Ile Pro Ser Asp Lys Gly Thr Tyr Gly Cys Arg Phe His Ser Asp 125 130 135  
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Asp	Gly	Ala	Pro	Arg	Phe	His	Gly	Arg	Val	Gly	Phe	Thr	Gly	Thr	Met	
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Pro	Ala	Thr	Asn	Val	Ser	Ile	Phe	Ile	Asn	Asn	Thr	Gln	Leu	Ser	Asp	
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Thr	Gly	Thr	Tyr	Gln	Cys	Leu	Val	Asn	Asn	Leu	Pro	Asp	Ile	Gly	Gly	
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Ala Ala Leu Ile Asn Leu Asn Val Ile Trp Met Val Thr Pro Leu Ser  
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Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln Met  
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Phe Asp Gly Ala Pro Arg Phe His Gly Arg Val Gly Phe Thr Gly Thr  
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Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro Ser  
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Ala Pro His Cys Gln Ile Gln Gly Ser Gln Asp Ile Gly Ser Asp Val  
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Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr Leu  
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Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr Gln  
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Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu Ser  
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Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser Thr  
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Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Asn Ile Gly  
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Ile Ala Leu Ile Leu Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn Lys  
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Trp Ser Asn Asn Pro Lys Val His Arg Asn Thr Glu Ser Val Ser His  
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Ile Pro Ser Ile Tyr Ala Asn Gly Thr His Leu Val Pro Gly Gln His  
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Lys Thr Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Met  
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Ser Arg Ser Asn Gly Ser Val Ser Arg Lys Pro Arg Pro Pro His Thr  
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Gly	Arg	Asn	Ile	Gly	Val	Thr	Gly	Leu	Thr	Val	Leu	Val	Pro	Pro	Ser
	130					135					140				
Ala	Pro	His	Cys	Gln	Ile	Gln	Gly	Ser	Gln	Asp	Ile	Gly	Ser	Asp	Val
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Ile	Leu	Leu	Cys	Ser	Ser	Glu	Glu	Gly	Ile	Pro	Arg	Pro	Thr	Tyr	Leu
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Trp	Glu	Lys	Leu	Asp	Asn	Thr	Leu	Lys	Leu	Pro	Pro	Thr	Ala	Thr	Gln
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Met Thr Arg Arg Arg Ser Ala Pro Ala Ser Trp Leu Leu Val Ser  
1 5 10 15  
  
ctg ctc ggt gtc gca aca tcc ctg gaa gtg tcc gag agc cca ggc agt 156  
Leu Leu Gly Val Ala Thr Ser Leu Glu Val Ser Glu Ser Pro Gly Ser  
20 25 30  
  
gtc cag gtg gcc cgg ggc cag aca gca gtc ctg ccc tgc gcc ttc tcc 204  
Val Gln Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Ala Phe Ser  
35 40 45  
  
acc agt gct gcc ctc ctg aac ctc aat gtc att tgg atg gtc att ccc 252  
Thr Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile Pro  
50 55 60  
  
ctc tcc aat gca aac cag ccc gaa cag gtc att ctt tat cag ggt gga 300  
Leu Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly  
65 70 75  
  
caa atg ttt gac ggc gcc ctc cgg ttc cac ggg agg gta gga ttt acc 348  
Gln Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe Thr  
80 85 90 95  
  
ggc acc atg cct gct acc aat gtc tcg atc ttc atc aat aac aca cag 396  
Gly Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln  
100 105 110  
  
ctg tca gat acg ggc acg tac cag tgc ttg gtg aat aac ctt cca gac 444  
Leu Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp  
115 120 125  
  
aga ggg ggc aga aac atc ggg gtc act ggc ctc aca gtg tta gtc ccc 492  
Arg Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro  
130 135 140  
  
cct tct gct cca caa tgc caa atc caa gga tcc cag gac ctc ggc agt 540  
Pro Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly Ser  
145 150 155  
  
gac gtc atc ctt ctg tgt agt tca gag gaa ggc atc cct cgg ccc acg 588

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Tyr	Leu	Trp	Glu	Lys 180	Leu	Asp	Asn	Thr	Leu	Lys 185	Leu	Pro	Pro	Thr	Ala 190	
act	cag	gac	cag	gtc	cag	gga	aca	gtc	acc	atc	cgg	aat	atc	agt	gcc	684
Thr	Gln	Asp	Gln	Val	Gln	Gly	Thr	Val	Thr	Ile	Arg	Asn	Ile	Ser	Ala 205	
ctc	tct	tcc	ggc	ctg	tac	cag	tgt	gtg	gct	tct	aat	gcc	atc	ggg	acc	732
Leu	Ser	Ser	Gly	Leu	Tyr	Gln	Cys 215	Val	Ala	Ser	Asn	Ala	Ile	Gly	Thr	
agc	acc	tgt	ctg	ctg	gac	ctc	cag	gtt	atc	tca	ccc	cag	ccc	cgg	agc	780
Ser	Thr	Cys	Leu	Leu	Asp	Leu	Gln	Val	Ile	Ser	Pro	Gln	Pro	Arg	Ser	
gtt	gga	gta	ata	gcc	gga	gcg	gtt	ggc	acc	ggc	gct	gtt	ctt	atc	gtc	828
Val	Gly	Val	Ile	Ala	Gly	Ala	Val	Gly	Thr	Gly	Ala	Val	Leu	Ile	Val 255	
atc	tgc	ctt	gca	cta	att	tca	ggg	gcg	ttc	ttt	tac	tgg	aga	agc	aaa	876
Ile	Cys	Leu	Ala	Leu	Ile	Ser	Gly	Ala	Phe	Phe	Tyr	Trp	Arg	Ser	Lys 270	
aac	aaa	gag	gag	gag	gag	gaa	gaa	att	cct	aat	gaa	atc	aga	gag	gat	924
Asn	Lys	Glu	Glu	Glu	Glu	Glu	Glu	Ile	Pro	Asn	Glu	Ile	Arg	Glu	Asp 285	
gat	ctt	ccc	cct	aaa	tgc	tct	tct	gcc	aaa	gcc	ttc	cac	acg	gag	ata	972
Asp	Leu	Pro	Pro	Lys	Cys	Ser	Ser	Ala	Lys	Ala	Phe	His	Thr	Glu	Ile	
tcc	tcc	tca	gaa	aat	aac	acg	ctg	acc	tct	tcc	aat	acc	tac	aac	agt	1020
Ser	Ser	Ser	Glu	Asn	Asn	Thr	Leu	Thr	Ser	Ser	Asn	Thr	Tyr	Asn	Ser	
cga	tac	tgg	aac	aac	aat	cca	aaa	ccc	cat	aga	aac	aca	gag	tct	ttc	1068
Arg	Tyr	Trp	Asn	Asn	Asn	Pro	Lys	Pro	His	Arg	Asn	Thr	Glu	Ser	Phe 335	
aac	cac	ttc	agt	gac	tta	cgc	cag	tct	ttc	tct	ggc	aat	gca	gtt	atc	1116
Asn	His	Phe	Ser	Asp	Leu	Arg	Gln	Ser	Phe	Ser	Gly	Asn	Ala	Val	Ile 350	
cca	tca	atc	tat	gca	aat	ggg	aac	cat	ctg	gtt	ttg	ggc	cca	cat	aag	1164
Pro	Ser	Ile	Tyr	Ala	Asn	Gly	Asn	His	Leu	Val	Leu	Gly	Pro	His	Lys	
act	ctg	gta	gtt	aca	gcc	aac	aga	ggg	tca	tca	cct	cag	gtc	ttg	ccc	1212
Thr	Leu	Val	Val	Thr	Ala	Asn	Arg	Gly	Ser	Ser	Pro	Gln	Val	Leu	Pro	
agg	aac	aat	ggc	tca	gtc	agc	agg	aag	cct	tgg	cct	caa	cac	act	cat	1260
Arg	Asn	Asn	Gly	Ser	Val	Ser	Arg	Lys	Pro	Trp	Pro	Gln	His	Thr	His	
tcc	tac	aca	gta	agc	caa	atg	acc	ctg	gag	cgc	atc	ggc	gca	gtg	cct	1308
Ser	Tyr	Thr	Val	Ser	Gln	Met	Thr	Leu	Glu	Arg	Ile	Gly	Ala	Val	Pro 415	

gtc atg gtg cct gcc cag agt cga gca ggg tcc ctg gta taggatgact 1357  
Val Met Val Pro Ala Gln Ser Arg Ala Gly Ser Leu Val  
420 425

gaggaaacca tgttcagaag agaataaatg gaccgcct 1395

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Gln Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Ala Phe Ser Thr  
35 40 45

Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile Pro Leu  
50 55 60

Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln  
65 70 75 80

Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe Thr Gly  
85 90 95

Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu  
100 105 110

Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Arg  
115 120 125

Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro  
130 135 140

Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly Ser Asp  
145 150 155 160

Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr  
165 170 175

Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr  
180 185 190

Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu  
195 200 205

Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser  
210 215 220

Thr Cys Leu Leu Asp Leu Gln Val Ile Ser Pro Gln Pro Arg Ser Val  
225 230 235 240

Gly Val Ile Ala Gly Ala Val Gly Thr Gly Ala Val Leu Ile Val Ile  
245 250 255

Cys Leu Ala Leu Ile Ser Gly Ala Phe Phe Tyr Trp Arg Ser Lys Asn  
260 265 270

Lys Glu Glu Glu Glu Glu Glu Ile Pro Asn Glu Ile Arg Glu Asp Asp  
275 280 285

Leu Pro Pro Lys Cys Ser Ser Ala Lys Ala Phe His Thr Glu Ile Ser  
290 295 300

Ser Ser Glu Asn Asn Thr Leu Thr Ser Ser Asn Thr Tyr Asn Ser Arg  
305 310 315 320

Tyr Trp Asn Asn Asn Pro Lys Pro His Arg Asn Thr Glu Ser Phe Asn  
325 330 335

His Phe Ser Asp Leu Arg Gln Ser Phe Ser Gly Asn Ala Val Ile Pro  
340 345 350

Ser Ile Tyr Ala Asn Gly Asn His Leu Val Leu Gly Pro His Lys Thr  
355 360 365

Leu Val Val Thr Ala Asn Arg Gly Ser Ser Pro Gln Val Leu Pro Arg  
370 375 380

Asn Asn Gly Ser Val Ser Arg Lys Pro Trp Pro Gln His Thr His Ser  
385 390 395 400

Tyr Thr Val Ser Gln Met Thr Leu Glu Arg Ile Gly Ala Val Pro Val  
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Met Val Pro Ala Gln Ser Arg Ala Gly Ser Leu Val  
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           1                          5                          10

tcg ctg ctc ggt gtc gca aca tcc ctg gaa gtg tcc gag agc cca ggc 98  
 Ser Leu Leu Gly Val Ala Thr Ser Leu Glu Val Ser Glu Ser Pro Gly  
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agt gtc cag gtg gcc cgg ggc cag aca gca gtc ctg ccc tgc gcc ttc 146  
 Ser Val Gln Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Ala Phe  
                           35                          40                          45

tcc acc agt gct gcc ctc ctg aac ctc aat gtc att tgg atg gtc att 194  
 Ser Thr Ser Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile  
                           50                          55                          60

ccc ctc tcc aat gca aac cag ccc gaa cag gtc att ctt tat cag ggt 242  
 Pro Leu Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly  
                           65                          70                          75

gga caa atg ttt gac ggc gcc ctc cgg ttc cac ggg agg gta gga ttt 290  
 Gly Gln Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe  
           80                          85                          90

acc ggc acc atg cct gct acc aat gtc tcg atc ttc atc aat aac aca 338  
 Thr Gly Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr  
 95                          100                          105                          110

cag ctg tca gat acg ggc acg tac cag tgc ttg gtg aat aac ctt cca 386  
 Gln Leu Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro  
                           115                          120                          125

gac aga ggg ggc aga aac atc ggg gtc act ggc ctc aca gtg tta gtc 434  
 Asp Arg Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val  
                           130                          135                          140

ccc cct tct gct cca caa tgc caa atc caa gga tcc cag gac ctc ggc 482  
 Pro Pro Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly  
                           145                          150                          155

agt gac gtc atc ctt ctg tgt agt tca gag gaa ggc atc cct cgg ccc 530  
 Ser Asp Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro  
           160                          165                          170

acg tac ctt tgg gag aag tta gat aat acg ctc aag cta cct cca aca 578  
 Thr Tyr Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr  
 175                          180                          185                          190

gcc act cag gac cag gtc cag gga aca gtc acc atc cgg aat atc agt 626  
 Ala Thr Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser  
                           195                          200                          205

gcc ctc tct tcc ggt ctg tac cag tgt gtg gct tct aat gcc atc ggg 674

Ala Leu Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly  
210 215 220

acc agc acc tgt ctg ctg gac ctc cag gtt atc tca ccc gtg cta gcc c 723  
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Gln Val Ala Arg Gly Gln Thr Ala Val Leu Pro Cys Ala Phe Ser Thr  
35 40 45

Ser Ala Ala Leu Leu Asn Leu Asn Val Ile Trp Met Val Ile Pro Leu  
50 55 60

Ser Asn Ala Asn Gln Pro Glu Gln Val Ile Leu Tyr Gln Gly Gly Gln  
65 70 75 80

Met Phe Asp Gly Ala Leu Arg Phe His Gly Arg Val Gly Phe Thr Gly  
85 90 95

Thr Met Pro Ala Thr Asn Val Ser Ile Phe Ile Asn Asn Thr Gln Leu  
100 105 110

Ser Asp Thr Gly Thr Tyr Gln Cys Leu Val Asn Asn Leu Pro Asp Arg  
115 120 125

Gly Gly Arg Asn Ile Gly Val Thr Gly Leu Thr Val Leu Val Pro Pro  
130 135 140

Ser Ala Pro Gln Cys Gln Ile Gln Gly Ser Gln Asp Leu Gly Ser Asp  
145 150 155 160

Val Ile Leu Leu Cys Ser Ser Glu Glu Gly Ile Pro Arg Pro Thr Tyr  
165 170 175

Leu Trp Glu Lys Leu Asp Asn Thr Leu Lys Leu Pro Pro Thr Ala Thr  
180 185 190

Gln Asp Gln Val Gln Gly Thr Val Thr Ile Arg Asn Ile Ser Ala Leu  
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Ser Ser Gly Leu Tyr Gln Cys Val Ala Ser Asn Ala Ile Gly Thr Ser  
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cta ata gtg ctc acc tat ggc cac ccc acc cta aaa aca cct gag agt 99  
Leu Ile Val Leu Thr Tyr Gly His Pro Thr Leu Lys Thr Pro Glu Ser  
15 20 25

gtg aca ggg acc tgg aaa gga gat gtg aag att cag tgc atc tat gat 147  
Val Thr Gly Thr Trp Lys Gly Asp Val Lys Ile Gln Cys Ile Tyr Asp  
30 35 40

ccc ctg aga ggc tac agg caa gtt ttg gtg aaa tgg ctg gta aga cac 195  
Pro Leu Arg Gly Tyr Arg Gln Val Leu Val Lys Trp Leu Val Arg His  
45 50 55 60

ggc tct gac tcc gtc acc atc ttc cta cgt gac tcc act gga gac cat 243  
Gly Ser Asp Ser Val Thr Ile Phe Leu Arg Asp Ser Thr Gly Asp His  
65 70 75

atc cag cag gca aag tac aga ggc cgc ctg aaa gtg agc cac aaa gtt 291  
Ile Gln Gln Ala Lys Tyr Arg Gly Arg Leu Lys Val Ser His Lys Val  
80 85 90

cca gga gat gtg tcc ctc caa ata aat acc ctg cag atg gat gac agg 339  
Pro Gly Asp Val Ser Leu Gln Ile Asn Thr Leu Gln Met Asp Asp Arg  
95 100 105

aat cac tat aca tgt gag gtc acc tgg cag act cct gat gga aac caa 387  
Asn His Tyr Thr Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln  
110 115 120

gta ata aga gat aag atc att gag ctc cgt gtt cgg aaa tat aat cca 435  
Val Ile Arg Asp Lys Ile Ile Glu Leu Arg Val Arg Lys Tyr Asn Pro  
125 130 135 140

cct aga atc aat act gaa gca cct aca acc ctg cac tcc tct ttg gaa 483  
Pro Arg Ile Asn Thr Glu Ala Pro Thr Thr Leu His Ser Ser Leu Glu  
145 150 155

gca	aca	act	ata	atg	agt	tca	acc	tct	gac	ttg	acc	act	aat	ggg	act	531
Ala	Thr	Thr	Ile	Met	Ser	Ser	Thr	Ser	Asp	Leu	Thr	Thr	Asn	Gly	Thr	
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gga	aaa	ctt	gag	gag	acc	att	gct	ggg	tca	ggg	agg	aac	ctg	cca	atc	579
Gly	Lys	Leu	Glu	Glu	Thr	Ile	Ala	Gly	Ser	Gly	Arg	Asn	Leu	Pro	Ile	
		175					180					185				
ttt	gcc	ata	atc	ttc	atc	atc	tcc	ctt	tgc	tgc	ata	gta	gct	gtc	acc	627
Phe	Ala	Ile	Ile	Phe	Ile	Ile	Ser	Leu	Cys	Cys	Ile	Val	Ala	Val	Thr	
	190					195					200					
ata	cct	tat	atc	ttg	ttc	cgc	tgc	agg	aca	ttc	caa	caa	gag	tat	gtc	675
Ile	Pro	Tyr	Ile	Leu	Phe	Arg	Cys	Arg	Thr	Phe	Gln	Gln	Glu	Tyr	Val	
205					210					215					220	
tat	gga	gtg	agc	agg	gtg	ttt	gcc	agg	aag	aca	agc	aac	tct	gaa	gaa	723
Tyr	Gly	Val	Ser	Arg	Val	Phe	Ala	Arg	Lys	Thr	Ser	Asn	Ser	Glu	Glu	
				225					230					235		
acc	aca	agg	gtg	act	acc	atc	gca	act	gat	gaa	cca	gat	tcc	cag	gct	771
Thr	Thr	Arg	Val	Thr	Thr	Ile	Ala	Thr	Asp	Glu	Pro	Asp	Ser	Gln	Ala	
			240					245					250			
ctg	att	agt	gac	tac	tct	gat	gat	cct	tgc	ctc	agc	cag	gag	tac	caa	819
Leu	Ile	Ser	Asp	Tyr	Ser	Asp	Asp	Pro	Cys	Leu	Ser	Gln	Glu	Tyr	Gln	
		255				260						265				
ata	acc	atc	aga	tca	aca	atg	tct	att	cct	gcc	tgc	tgaacacagt	tt			867
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<400> 14

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			20					25					30		
Trp	Lys	Gly	Asp	Val	Lys	Ile	Gln	Cys	Ile	Tyr	Asp	Pro	Leu	Arg	Gly
		35					40					45			
Tyr	Arg	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Arg	His	Gly	Ser	Asp	Ser
	50					55					60				
Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Thr	Gly	Asp	His	Ile	Gln	Gln	Ala
65					70					75					80
Lys	Tyr	Arg	Gly	Arg	Leu	Lys	Val	Ser	His	Lys	Val	Pro	Gly	Asp	Val
				85					90					95	

-21-

Ser Leu Gln Ile Asn Thr Leu Gln Met Asp Asp Arg Asn His Tyr Thr  
100 105 110

Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Ile Arg Asp  
115 120 125

Lys Ile Ile Glu Leu Arg Val Arg Lys Tyr Asn Pro Pro Arg Ile Asn  
130 135 140

Thr Glu Ala Pro Thr Thr Leu His Ser Ser Leu Glu Ala Thr Thr Ile  
145 150 155 160

Met Ser Ser Thr Ser Asp Leu Thr Thr Asn Gly Thr Gly Lys Leu Glu  
165 170 175

Glu Thr Ile Ala Gly Ser Gly Arg Asn Leu Pro Ile Phe Ala Ile Ile  
180 185 190

Phe Ile Ile Ser Leu Cys Cys Ile Val Ala Val Thr Ile Pro Tyr Ile  
195 200 205

Leu Phe Arg Cys Arg Thr Phe Gln Gln Glu Tyr Val Tyr Gly Val Ser  
210 215 220

Arg Val Phe Ala Arg Lys Thr Ser Asn Ser Glu Glu Thr Thr Arg Val  
225 230 235 240

Thr Thr Ile Ala Thr Asp Glu Pro Asp Ser Gln Ala Leu Ile Ser Asp  
245 250 255

Tyr Ser Asp Asp Pro Cys Leu Ser Gln Glu Tyr Gln Ile Thr Ile Arg  
260 265 270

Ser Thr Met Ser Ile Pro Ala Cys  
275 280

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Ile	Val	Leu	Thr	Tyr	Gly	His	Pro	Thr	Leu	Lys	Thr	Pro	Glu	Ser	Val	
	15					20					25					
aca	ggg	acc	tgg	aaa	gga	gat	gtg	aag	att	cag	tgc	atc	tat	gat	ccc	145
Thr	Gly	Thr	Trp	Lys	Gly	Asp	Val	Lys	Ile	Gln	Cys	Ile	Tyr	Asp	Pro	
	30				35					40					45	
ctg	aga	ggc	tac	agg	caa	gtt	ttg	gtg	aaa	tgg	ctg	gta	aga	cac	ggc	193
Leu	Arg	Gly	Tyr	Arg	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Arg	His	Gly	
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tct	gac	tcc	gtc	acc	atc	ttc	cta	cgt	gac	tcc	act	gga	gac	cat	atc	241
Ser	Asp	Ser	Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Thr	Gly	Asp	His	Ile	
			65					70					75			
cag	cag	gca	aag	tac	aga	ggc	cgc	ctg	aaa	gtg	agc	cac	aaa	gtt	cca	289
Gln	Gln	Ala	Lys	Tyr	Arg	Gly	Arg	Leu	Lys	Val	Ser	His	Lys	Val	Pro	
		80					85					90				
gga	gat	gtg	tcc	ctc	caa	ata	aat	acc	ctg	cag	atg	gat	gac	agg	aat	337
Gly	Asp	Val	Ser	Leu	Gln	Ile	Asn	Thr	Leu	Gln	Met	Asp	Asp	Arg	Asn	
	95					100					105					
cac	tat	aca	tgt	gag	gtc	acc	tgg	cag	act	cct	gat	gga	aac	caa	gta	385
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tatctatatc	ataatatgta	catttatatt	ggctcatgtc	caatatgacc	gccatgttga	8400
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atcatcatca ttgagtttaa acgatccaga catgataaga tacattgatg agtttggaca    9960
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cgactctaga                                     10330

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<210> 25
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<213> Artificial Sequence

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<220>
<223> LV43-XM087714f primer

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<400> 25
tgctgacgag agatggtgg                                     19

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<210> 26
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<212> DNA
<213> Artificial Sequence

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<220>
<223> LV44-XM087714b primer

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<400> 26
ccacagcctt tagatgacgg                                     20

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<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

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<220>
<223> LV49-XM087714f primer

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<400> 27
gggggtacct gctgacgaga gatggtg                                     27

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<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

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<220>
<223> LV48-XM087714b primer

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<400> 28

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cggctagccc gggtagaac acgtc 25

<210> 29  
<211> 20  
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<220>  
<223> LV50-XP087460f primer

<400> 29  
tttccatctg aggcaagaag 20

<210> 30  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> LV60-hsB7-H5b primer

<400> 30  
ttcctcatgt cctataccaa gg 22

<210> 31  
<211> 30  
<212> DNA  
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<220>  
<223> LV56-sec-hsB7-H5f primer

<400> 31  
ggggtaccat gtctctggtg gaacttttgc 30

<210> 32  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> LV57-sec-hsB7-H5b primer

<400> 32  
cggctagccc aatgttcctg ggctgg 26

<210> 33  
<211> 17  
<212> DNA  
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<220>  
<223> JS7-mB7-H5f primer

<400> 33  
atgactcggc ggcgctc 17

<210> 34  
<211> 23  
<212> DNA  
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<220>  
<223> JS8-mB7-H5r primer

<400> 34  
ctataccagg gaccctgctc gac

23

<210> 35  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> MSt-1mB7-H5for primer

<400> 35  
ggggtacat gactcggcgg cgctcc

26

<210> 36  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> MSt-2mB7-H5rev primer

<400> 36  
gggctagcac gggtagagata acctggag

28

<210> 37  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> LV80-mC18f

<400> 37  
gtagcttcaa ataggatgga g

21

<210> 38  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> LV81-mC18b

<400> 38  
aaactgtgtt cagcaggcag

20

<210> 39  
<211> 26

<212> DNA  
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<220>  
<223> LV82-mC18f primer

<400> 39  
gggtaccagg atggagatct catcag

26

<210> 40  
<211> 23  
<212> DNA  
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<220>  
<223> LV83-mC18b primer

<400> 40  
ggctagcagg ttcctccctg aac

23

<210> 41  
<211> 1210  
<212> DNA  
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<220>  
<221> CDS  
<222> (6)..(1202)

<400> 41  
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Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val  
1 5 10 15

50

gac act tat ggc cgt ccc atc ctg gaa gtg cca gag agt gta aca gga  
Asp Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly  
20 25 30

98

cct tgg aaa ggg gat gtg aat ctt ccc tgc acc tat gac ccc ctg caa  
Pro Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln  
35 40 45

146

ggc tac acc caa gtc ttg gtg aag tgg ctg gta caa cgt ggc tca gac  
Gly Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp  
50 55 60

194

cct gtc acc atc ttt cta cgt gac tct tct gga gac cat atc cag cag  
Pro Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln  
65 70 75

242

gca aag tac cag ggc cgc ctg cat gtg agc cac aag gtt cca gga gat  
Ala Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp  
80 85 90 95

290

gta tcc ctc caa ttg agc acc ctg gag atg gat gac cgg agc cac tac  
Val Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr  
100 105 110

338

acg tgt gaa gtc acc tgg cag act cct gat ggc aac caa gtc gtg aga

386

Thr	Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro	Asp	Gly	Asn	Gln	Val	Val	Arg	
			115					120					125			
gat	aag	att	act	gag	ctc	cgt	gtc	cag	aaa	ctc	tct	gtc	tcc	aag	ccc	434
Asp	Lys	Ile	Thr	Glu	Leu	Arg	Val	Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	
		130					135					140				
aca	gtg	aca	act	ggc	agc	ggg	tat	ggc	ttc	acg	gtg	ccc	cag	gga	atg	482
Thr	Val	Thr	Thr	Gly	Ser	Gly	Tyr	Gly	Phe	Thr	Val	Pro	Gln	Gly	Met	
	145					150					155					
agg	att	agc	ctt	caa	tgc	cag	gct	cgg	ggg	tct	cct	ccc	atc	agt	tat	530
Arg	Ile	Ser	Leu	Gln	Cys	Gln	Ala	Arg	Gly	Ser	Pro	Pro	Ile	Ser	Tyr	
160					165					170					175	
att	tgg	tat	aag	caa	cag	act	aat	aac	cag	gaa	ccc	atc	aaa	gta	gca	578
Ile	Trp	Tyr	Lys	Gln	Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	
				180					185					190		
acc	cta	agt	acc	tta	ctc	ttc	aag	cct	gcg	gtg	ata	gcc	gac	tca	ggc	626
Thr	Leu	Ser	Thr	Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	
			195					200					205			
tcc	tat	ttc	tgc	act	gcc	aag	ggc	cag	gtt	ggc	tct	gag	cag	cac	agc	674
Ser	Tyr	Phe	Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	
		210					215					220				
gac	att	gtg	aag	ttt	gtg	gtc	aaa	gac	tcc	tca	aag	cta	ctc	aag	acc	722
Asp	Ile	Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	
	225					230					235					
aag	act	gag	gca	cct	aca	acc	atg	aca	tac	ccc	ttg	aaa	gca	aca	tct	770
Lys	Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	
240				245						250					255	
aca	gtg	aag	cag	tcc	tgg	gac	tgg	acc	act	gac	atg	gat	ggc	tac	ctt	818
Thr	Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	Leu	
			260					265					270			
gga	gag	acc	agt	gct	ggg	cca	gga	aag	agc	ctg	cct	gtc	ttt	gcc	atc	866
Gly	Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	Ala	Ile	
		275						280					285			
atc	ctc	atc	atc	tcc	ttg	tgc	tgt	atg	gtg	gtt	ttt	acc	atg	gcc	tat	914
Ile	Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	Met	Ala	Tyr	
		290				295					300					
atc	atg	ctc	tgt	cgg	aag	aca	tcc	caa	caa	gag	cat	gtc	tac	gaa	gca	962
Ile	Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	Val	Tyr	Glu	Ala	
	305					310					315					
gcc	agg	gca	cat	gcc	aga	gag	gcc	aac	gac	tct	gga	gaa	acc	atg	agg	1010
Ala	Arg	Ala	His	Ala	Arg	Glu	Ala	Asn	Asp	Ser	Gly	Glu	Thr	Met	Arg	
320					325					330					335	
gtg	gcc	atc	ttc	gca	agt	ggc	tgc	tcc	agt	gat	gag	cca	act	tcc	cag	1058
Val	Ala	Ile	Phe	Ala	Ser	Gly	Cys	Ser	Ser	Asp	Glu	Pro	Thr	Ser	Gln	
				340				345						350		
aat	ctg	ggc	aac	aac	tac	tct	gat	gag	ccc	tgc	ata	gga	cag	gag	tac	1106
Asn	Leu	Gly	Asn	Asn	Tyr	Ser	Asp	Glu	Pro	Cys	Ile	Gly	Gln	Glu	Tyr	
			355					360					365			



cag atc atc gcc cag atc aat ggc aac tac gcc cgc ctg ctg gac aca 1154  
Gln Ile Ile Ala Gln Ile Asn Gly Asn Tyr Ala Arg Leu Leu Asp Thr  
370 375 380

gtt cct ctg gat tat gag ttt ctg gcc act gag ggc aaa agt gtc tgt 1202  
Val Pro Leu Asp Tyr Glu Phe Leu Ala Thr Glu Gly Lys Ser Val Cys  
385 390 395

taaaaatg 1210

<210> 42  
<211> 399  
<212> PRT  
<213> homo sapiens

<400> 42

Met Gly Ile Leu Leu Gly Leu Leu Leu Leu Gly His Leu Thr Val Asp  
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Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro  
20 25 30

Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly  
35 40 45

Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro  
50 55 60

Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala  
65 70 75 80

Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val  
85 90 95

Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr  
100 105 110

Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp  
115 120 125

Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr  
130 135 140

Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg  
145 150 155 160

Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile  
165 170 175

Trp	Tyr	Lys	Gln	Gln	Thr	Asn	Asn	Gln	Glu	Pro	Ile	Lys	Val	Ala	Thr
			180					185					190		
Leu	Ser	Thr	Leu	Leu	Phe	Lys	Pro	Ala	Val	Ile	Ala	Asp	Ser	Gly	Ser
		195					200					205			
Tyr	Phe	Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp
	210					215					220				
Ile	Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys
225					230					235					240
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	Thr
				245					250					255	
Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	Leu	Gly
			260					265					270		
Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Ser	Leu	Pro	Val	Phe	Ala	Ile	Ile
		275					280					285			
Leu	Ile	Ile	Ser	Leu	Cys	Cys	Met	Val	Val	Phe	Thr	Met	Ala	Tyr	Ile
	290					295					300				
Met	Leu	Cys	Arg	Lys	Thr	Ser	Gln	Gln	Glu	His	Val	Tyr	Glu	Ala	Ala
305					310					315					320
Arg	Ala	His	Ala	Arg	Glu	Ala	Asn	Asp	Ser	Gly	Glu	Thr	Met	Arg	Val
				325					330					335	
Ala	Ile	Phe	Ala	Ser	Gly	Cys	Ser	Ser	Asp	Glu	Pro	Thr	Ser	Gln	Asn
			340					345					350		
Leu	Gly	Asn	Asn	Tyr	Ser	Asp	Glu	Pro	Cys	Ile	Gly	Gln	Glu	Tyr	Gln
		355					360					365			
Ile	Ile	Ala	Gln	Ile	Asn	Gly	Asn	Tyr	Ala	Arg	Leu	Leu	Asp	Thr	Val
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Pro	Leu	Asp	Tyr	Glu	Phe	Leu	Ala	Thr	Glu	Gly	Lys	Ser	Val	Cys	
385					390					395					

<210> 43  
 <211> 844  
 <212> DNA  
 <213> homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(843)

<220>  
 <221> misc\_feature  
 <222> (513)..(513)  
 <223> T at position 513 might be a C (silent mutation)

<400> 43  
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 1 5 10 15  
 act tat ggc cgt ccc atc ctg gaa gtg cca gag agt gta aca gga cct 96  
 Thr Tyr Gly Arg Pro Ile Leu Glu Val Pro Glu Ser Val Thr Gly Pro  
 20 25 30  
 tgg aaa ggg gat gtg aat ctt ccc tgc acc tat gac ccc ctg caa ggc 144  
 Trp Lys Gly Asp Val Asn Leu Pro Cys Thr Tyr Asp Pro Leu Gln Gly  
 35 40 45  
 tac acc caa gtc ttg gtg aag tgg ctg gta caa cgt ggc tca gac cct 192  
 Tyr Thr Gln Val Leu Val Lys Trp Leu Val Gln Arg Gly Ser Asp Pro  
 50 55 60  
 gtc acc atc ttt cta cgt gac tct tct gga gac cat atc cag cag gca 240  
 Val Thr Ile Phe Leu Arg Asp Ser Ser Gly Asp His Ile Gln Gln Ala  
 65 70 75 80  
 aag tac cag ggc cgc ctg cat gtg agc cac aag gtt cca gga gat gta 288  
 Lys Tyr Gln Gly Arg Leu His Val Ser His Lys Val Pro Gly Asp Val  
 85 90 95  
 tcc ctc caa ttg agc acc ctg gag atg gat gac cgg agc cac tac acg 336  
 Ser Leu Gln Leu Ser Thr Leu Glu Met Asp Asp Arg Ser His Tyr Thr  
 100 105 110  
 tgt gaa gtc acc tgg cag act cct gat ggc aac caa gtc gtg aga gat 384  
 Cys Glu Val Thr Trp Gln Thr Pro Asp Gly Asn Gln Val Val Arg Asp  
 115 120 125  
 aag att act gag ctc cgt gtc cag aaa ctc tct gtc tcc aag ccc aca 432  
 Lys Ile Thr Glu Leu Arg Val Gln Lys Leu Ser Val Ser Lys Pro Thr  
 130 135 140  
 gtg aca act ggc agc ggt tat ggc ttc acg gtg ccc cag gga atg agg 480  
 Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg  
 145 150 155 160  
 att agc ctt caa tgc cag gct cgg ggt tct cct ccc atc agt tat att 528  
 Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile  
 165 170 175  
 tgg tat aag caa cag act aat aac cag gaa ccc atc aaa gta gca acc 576  
 Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr  
 180 185 190  
 cta agt acc tta ctc ttc aag cct gcg gtg ata gcc gac tca ggc tcc 624  
 Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser  
 195 200 205

tat	ttc	tgc	act	gcc	aag	ggc	cag	gtt	ggc	tct	gag	cag	cac	agc	gac	672
Tyr	Phe	Cys	Thr	Ala	Lys	Gly	Gln	Val	Gly	Ser	Glu	Gln	His	Ser	Asp	
	210					215					220					
att	gtg	aag	ttt	gtg	gtc	aaa	gac	tcc	tca	aag	cta	ctc	aag	acc	aag	720
Ile	Val	Lys	Phe	Val	Val	Lys	Asp	Ser	Ser	Lys	Leu	Leu	Lys	Thr	Lys	
	225				230					235					240	
act	gag	gca	cct	aca	acc	atg	aca	tac	ccc	ttg	aaa	gca	aca	tct	aca	768
Thr	Glu	Ala	Pro	Thr	Thr	Met	Thr	Tyr	Pro	Leu	Lys	Ala	Thr	Ser	Thr	
				245					250					255		
gtg	aag	cag	tcc	tgg	gac	tgg	acc	act	gac	atg	gat	ggc	tac	ctt	gga	816
Val	Lys	Gln	Ser	Trp	Asp	Trp	Thr	Thr	Asp	Met	Asp	Gly	Tyr	Leu	Gly	
			260					265					270			
gag	acc	agt	gct	ggg	cca	gga	aag	cta	g							844
Glu	Thr	Ser	Ala	Gly	Pro	Gly	Lys	Leu								
		275					280									

<210> 44  
 <211> 281  
 <212> PRT  
 <213> homo sapiens

<400> 44

Met	Gly	Ile	Leu	Leu	Gly	Leu	Leu	Leu	Leu	Gly	His	Leu	Thr	Val	Asp
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			20					25					30		
Trp	Lys	Gly	Asp	Val	Asn	Leu	Pro	Cys	Thr	Tyr	Asp	Pro	Leu	Gln	Gly
		35					40					45			
Tyr	Thr	Gln	Val	Leu	Val	Lys	Trp	Leu	Val	Gln	Arg	Gly	Ser	Asp	Pro
	50					55					60				
Val	Thr	Ile	Phe	Leu	Arg	Asp	Ser	Ser	Gly	Asp	His	Ile	Gln	Gln	Ala
65					70					75					80
Lys	Tyr	Gln	Gly	Arg	Leu	His	Val	Ser	His	Lys	Val	Pro	Gly	Asp	Val
				85					90					95	
Ser	Leu	Gln	Leu	Ser	Thr	Leu	Glu	Met	Asp	Asp	Arg	Ser	His	Tyr	Thr
			100					105					110		
Cys	Glu	Val	Thr	Trp	Gln	Thr	Pro	Asp	Gly	Asn	Gln	Val	Val	Arg	Asp
		115					120					125			
Lys	Ile	Thr	Glu	Leu	Arg	Val	Gln	Lys	Leu	Ser	Val	Ser	Lys	Pro	Thr
	130					135					140				

Val Thr Thr Gly Ser Gly Tyr Gly Phe Thr Val Pro Gln Gly Met Arg  
145 150 155 160

Ile Ser Leu Gln Cys Gln Ala Arg Gly Ser Pro Pro Ile Ser Tyr Ile  
165 170 175

Trp Tyr Lys Gln Gln Thr Asn Asn Gln Glu Pro Ile Lys Val Ala Thr  
180 185 190

Leu Ser Thr Leu Leu Phe Lys Pro Ala Val Ile Ala Asp Ser Gly Ser  
195 200 205

Tyr Phe Cys Thr Ala Lys Gly Gln Val Gly Ser Glu Gln His Ser Asp  
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